

Figure 1

10 30 50
 CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCACAAAATACACCGA
 70 90 110
 CGATGCCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
 130 150 170
 CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGCGCTTCGGGGGCCCCGAAAAGG
M E O R G O N A P A A S G A R K R
 190 210 230
 CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
 250 270 290
 CTTGTGCTCGTTGTGCGCCGCGGTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T
 310 330 350
 CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCAACAAGAGGTCCAGCCCCCTCA
 Q Q D L A P Q Q R A A P Q Q K R S S P S
 370 390 410
 GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCTCTGC
 E G L C P P G H H I S E D G R D C I S C
 430 450 470
 AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCCTGCACCC
 K Y G Q D Y S T H W N D L L F C L R C T
 490 510 530
 AGGTGTGATTGAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
 R C D S G E V E L S P C T T T R N T V C
 550 570 590
 CAGTGCGAAGAAGGCACCTTCCGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
 Q C E E G T F R E E D S P E M C R K C R
 610 630 650
 ACAGGGTGTCCCAGAGGGATGGTCAAGGTGCGGTGATTGTACACCCTGGAGTGACATCGAA
 T G C P R G M V K V G D C T P W S D I E
 670 690 710
 TGTGTCCACAAAGAATCAGGCATCATATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
 C V H K E S G I I I G V T V A A V V L I
 730 750 770
 GTGGCTGTGTTTGTGTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
 790 810 830
 ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
 I C S G G G G D P E R V D R S S Q R P G
 850 870 890
 GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
 A E D N V L N E I V S I L Q P T Q V P E
 910 930 950
 CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
 Q E M E V Q E P A E P T G V N M L S P G
 970 990 1010
 GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
 E S E H L L E P A E A E R S Q R R L L
 1030 1050 1070

062700-034500

Figure 1 (continued)

GTTCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V P A N E G D P T E T L R Q C F D D F A
1090 1110 1130
GACTTGGTGGCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D L V P F D S W E P L M R K L G L M D N
1150 1170 1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGACACGATGCTG
E I K V A K A E A A G H R D T L Y T M L
1210 1230 1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I K W V N K T G R D A S V H T L L D A L
1270 1290 1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E T L G E R L A K Q K I E D H L L S S G
1330 1350 1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K F M Y L E G N A D S A M S *
1390 1410 1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCACTGGACTCCAGTC
1450 1470 1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAACTCTCCCATCCAACA
1510 1530 1550
TCACCCAGTGGATGGAACATCCTGTAACCTTTTCACTGCACTTGGCATTATTTTTATAAGC
1570 1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAA

BB47ED-EB524060

Figure 2

1 M-LG-----I W T L L P L V L h Fas protein
1 MGLS-----T V P D L L L P L h TNFR I Protein
1 MQR-----P R G C A A V A A DR3 protein
1 MQRG Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L HLYBX88XXprotein

13 T S V A R L S S K S V N A Q V T D I N S K G L E L R K T V T T V E T Q N L E G L h Fas protein
14 V L L E L L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G K Y I H - - h TNFR I Protein
14 A L L E L L L G A R A Q G - - - - - G T R S P R - C D C A - G D F - H - - DR3 protein
41 V V A A V E L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G L HLYBX88XXprotein

53 H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T h Fas protein
52 P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S F T A h TNFR I Protein
41 K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A DR3 protein
81 - - - - - C P P G H H I S E D - - - - - G R D C I S C K Y G Q D Y S HLYBX88XXprotein

93 D K A E F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N h Fas protein
92 S E N H L R - H C L S C S K C R K Z M G Q V E I S S C T V D R D T V C G C R K N h TNFR I Protein
81 W E N H H M S E C A R C Q A C D E Q A S O V A L E N C S A V A D T R C G C K P G DR3 protein
105 T E W N D L L F C L R C T R C D - - S G E V E L S P C T T T R N T V C Q C E E G HLYBX88XXprotein

133 F F - - - - - C N S T V - - - - - C E H C D P C T K - - - - - h Fas protein
131 Q Y R E Y W S E N L F Q C - - - - - F N C S L C L N - G T V H - - - - - L S C Q E h TNFR I Protein
121 W F V E C - - - - - Q V S O C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R DR3 protein
143 T E R E - - - - - E D S P E M C R K C - - - - - R T G C P R HLYBX88XXprotein

149 - - - - - C E H G I I - - - - - K E C - - - - - T L T S N T K C K E - - - h Fas protein
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S I E C T F L C L P Q I E h TNFR I Protein
158 R D T D C G T C L P G E Y Z H G D G C V S C P T S T L G - S C P E R C A A V C G DR3 protein
163 G M V R V G D C T E - - - - - W S D I E C V - - - - - H R E S G I I I G HLYBX88XXprotein

168 - - - - - E G S R S N L G W - - - - - L C L L - L L P I P L I V - - - - - W h Fas protein
201 N Y K G T E D S G T T V L L P L V I F F G L C L L S L L F I G L M Y R Y Q R - W h TNFR I Protein
197 W R Q - - - - - M F W V Q V L L A G L V V P L L L G A T L T Y T Y R H C W DR3 protein
189 - - - - - V T V A A V V L I V A V F - - - - - V C K S L L W K K V L P Y L K G I C S HLYBX88XXprotein

190 V E R E V Q K T C R R H F K E N Q G S H E S - - - - - h Fas protein
240 - E S E L Y S I V C G R S T P E K E G E L E G T T T K P L A P N P S F S P T P G h TNFR I Protein
229 - P H R P L - V F A D E A G M E A L T P P P A T H L S P L D S A H T L L A P P D DR3 protein
221 - - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q E T Q HLYBX88XXprotein

213 - - - - - h Fas protein
279 F T P T L G F S P V E S S T F T S S S T Y T P G D - C P N F A A P R R E V A P P h TNFR I Protein
267 S S E K I C T V Q L V G N S W T P G Y B E T Q E A L C P Q V T W S W D Q L - - - DR3 protein
255 V P E Q E M E V O E P A E - - - - - P T G V N M L S P G - - - - - E S E H L - - - HLYBX88XXprotein

213 - - - - - P T L N P E T V A I N L - - - - - S D V D L S K Y I T T I A G V M h Fas protein
313 Y Q G A D P I L A T A L A S D P I P N L Q K W E D S A H K P Q S L D T D D P A h TNFR I Protein
305 S R A L G P A A A P T L S E - - - - - E S P A G S P A M M L Q P G B Q DR3 protein
283 - - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R O HLYBX88XXprotein

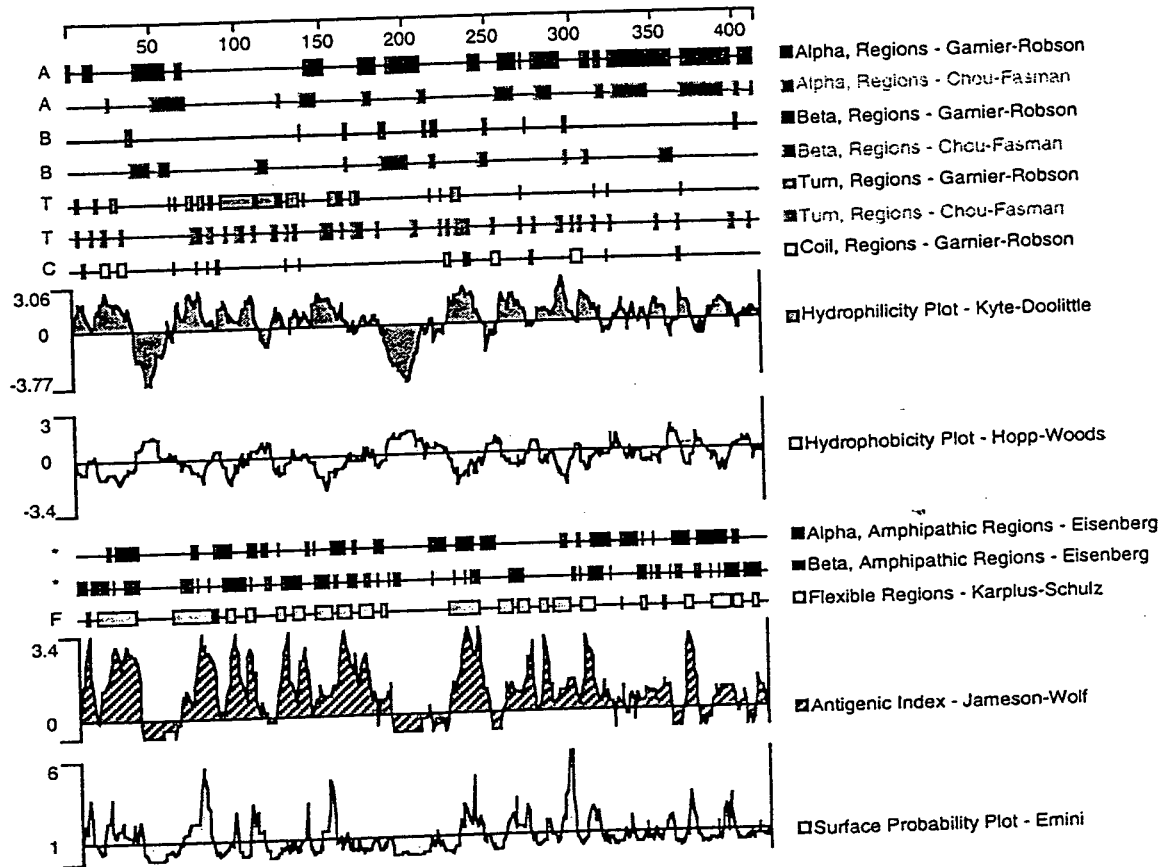
241 T L S Q V - - - - - K G F V R R N G V N E A K I D E I K N D N V Q D T A h Fas protein
358 T L V A V V E N V P P L R W K E F V R R L G L S D H E I D R L E L Q N C R C L R h TNFR I Protein
335 - L Y D V M D A V P A R R W K E F V R C L G L R E A E I E A V E V E I G R - F R DR3 protein
312 C F D D F A D L V E F D S W E P L M R K L G L M D N E I - K V A K A E A A G H R HLYBX88XXprotein

272 E O K V Q L L R N U H O L H G K R E A - Y D T L I K D L K K A N L C T L A E K I h Fas protein
398 E A Q Y S M L A T E R R R T P F R E A T L E L L G R V L R D M D L L G C L E D I h TNFR I Protein
373 D O O Y E M L K R E R O Q Q P - - - - - A G L G A V Y A A L E R M G L D G C V E D L DR3 protein
351 D T L Y T M L I K E V N K T G P - D A S V H T L L D A E L T L G E R L A K Q K I HLYBX88XXprotein

311 Q T I I E K D I T S D S E N S M F R N E I Q S L V h Fas protein
438 E E A L - - - - - C G P A A L P P A P S L L R h TNFR I Protein
419 - - - - - R S R L Q R G P DR3 protein
390 E D H L L S S G K F M Y L E G N - - - - - A D S A M S HLYBX88XXprotein

Decorations: Decoration #1: Shade (with solid black) residues that match the Consensus exactly.

Figure 3



BB-100-23524060

Figure 4

HAPBU13R

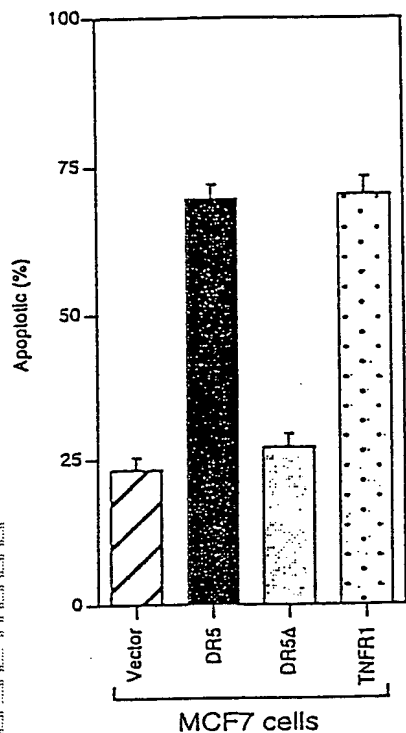
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51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
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151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCC GACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG

HSBBU76R

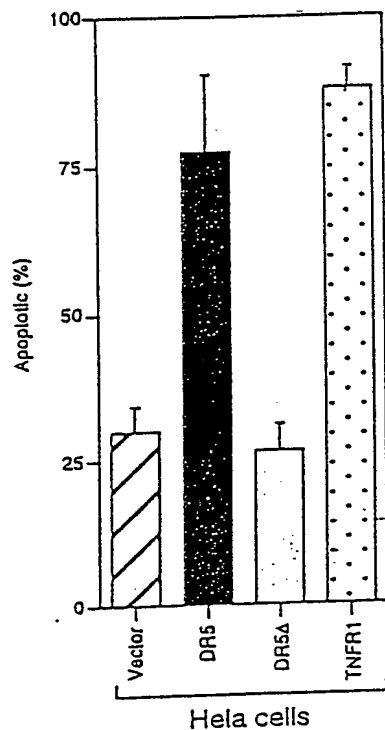
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51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT

Figure 5

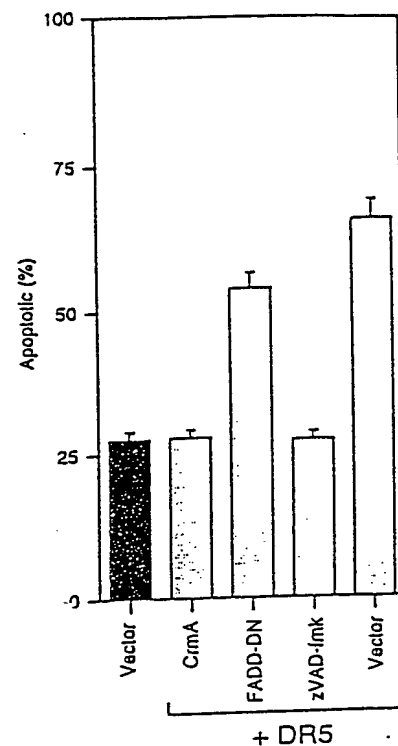
A



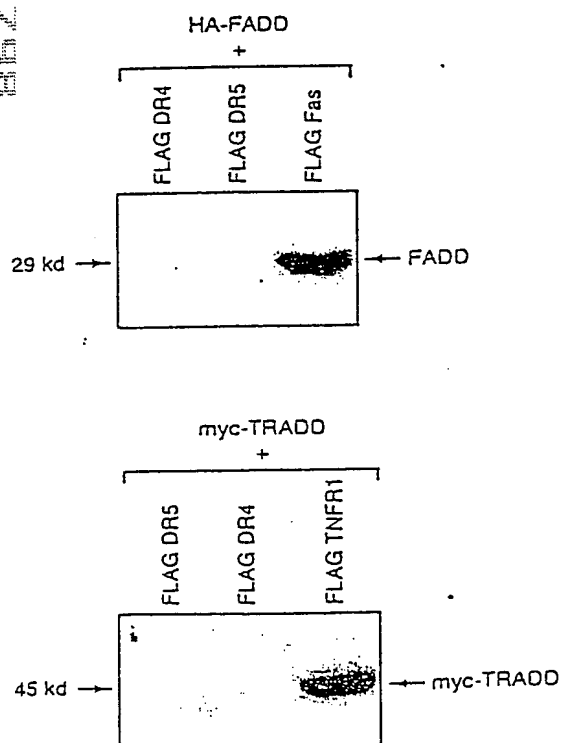
B



C



D



E

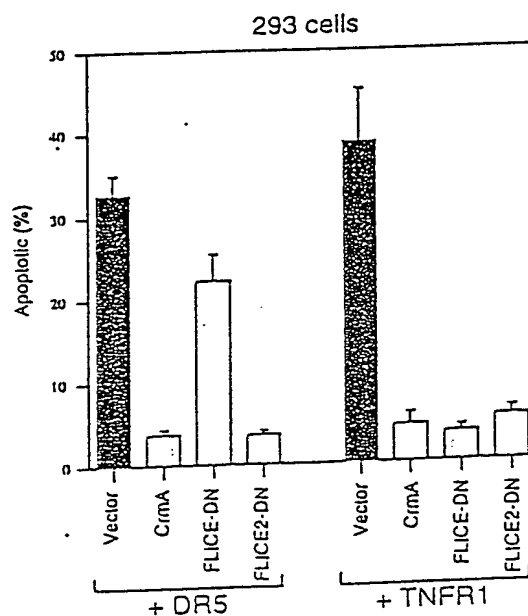
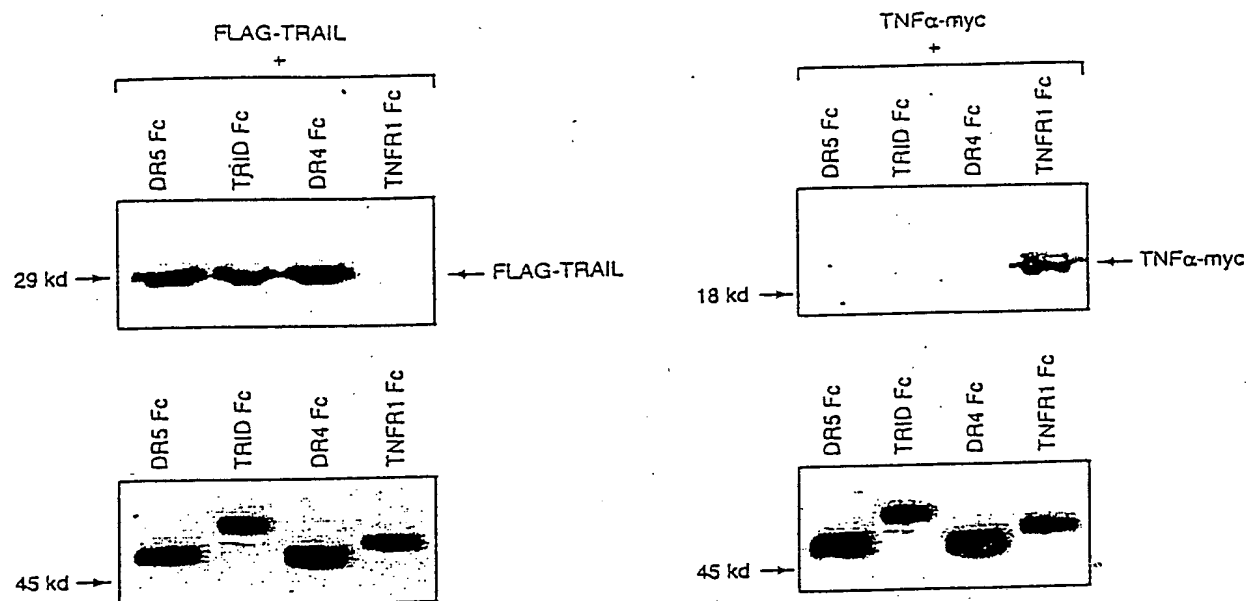
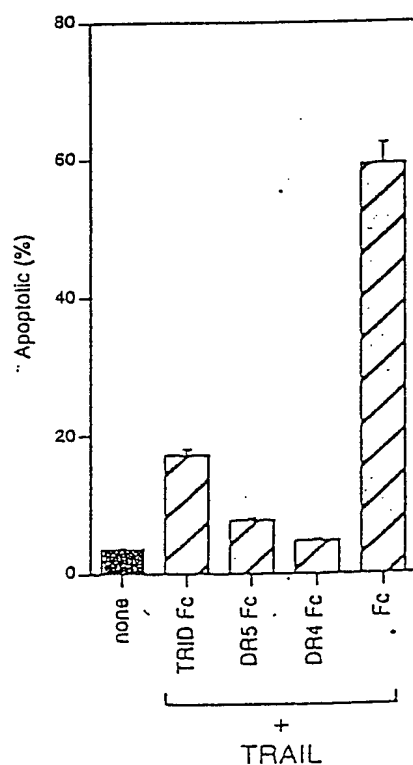


Figure 6

A



B



C

